WHAT IS CLAIMED IS:

1. A protein profiling system, comprising:

a protein fractionation unit that separates a protein content of a tissue or specimen sample from a respective subject into protein subgroups;

a mass spectrometer that independently performs mass spectroscopy on each of the protein subgroups from the respective subject's sample, and outputs respective mass spectra subgroup data;

a protein data processing unit that analyzes the mass spectra subgroup data to create a protein profile for the tissue or specimen sample, and identifies protein patterns associated with subject characteristics based on the protein profile and information received on the respective subjects; and

a database that stores the protein profile and the identified protein patterns.

2. The system of claim 1, wherein the subject characteristics comprise predetermined biological conditions.

3. The system of claim 2, wherein at least one of the predetermined biological conditions comprises a predetermined disease.

4.   The system of claim 1, wherein the protein data processing unit identifies the protein patterns associated with subject characteristics by comparing protein profiles from a plurality of subjects having a common subject characteristic.

5.   The system of claim 1, wherein the protein data processing unit uses a neural network to identify the protein patterns associated with subject characteristics.

6.   The system of claim 1, wherein the protein data processing unit uses a peak analysis techniques to identify the protein patterns associated with subject characteristics.

7.   A diagnostic system, comprising:

a database that stores protein patterns associated with subject characteristics;

a protein data processing unit that separates a protein content of a tissue or specimen sample from a respective subject into protein subgroups;

a mass spectrometer that independently performs mass spectroscopy on each of the protein subgroups from the respective subject's sample, and outputs respective mass spectra subgroup data; and

a diagnostic unit that analyzes the mass spectra subgroup data to create a protein profile for the tissue or specimen sample, and that compares the protein profile with the stored protein patterns to predict the existence or non-existence of at least one subject characteristic in the respective subject.

8.   The system of claim 7, wherein the at least one subject characteristic comprises a predetermined biological condition.

9.   The system of claim 8, wherein the predetermined biological condition comprises a disease.

10.   A biomarker diagnostic method, comprising the steps of:

collecting a tissue or specimen sample;

fractioning protein content from the sample into protein subgroups;

separately performing mass spectroscopy on each of said protein subgroups and storing resulting mass spectra subgroup data;

analyzing said resulting mass spectra subgroup data to yield a protein profile for said sample.

11.   The method of claim 10, wherein said protein profile comprises a comprehensive protein profile.

12.   The method of claim 10, wherein said analyzing step comprises analyzing said resulting mass spectra subgroup data using an artificial neural network.

13. The method of claim 10, wherein said separately performing step comprises collecting data points corresponding to said mass spectra subgroup.

14. The method of claim 10, wherein said analyzing step comprises determining data points which yield useful diagnostic information.

15. The method of claim 10, wherein said separately performing step comprises collecting data points corresponding to said mass spectra subgroup, and said analyzing step comprises determining data points which yield useful diagnostic information.

16. The method of claim 15, wherein said data points include data points other than peaks of said mass spectra subgroup.

17. A method for rapidly identifying protein biomarkers, comprising the steps of:

collecting a diseased tissue or specimen sample from at least one patient;

fractionating protein content from said diseased tissue or specimen sample into protein subgroups;

separately performing mass spectroscopy on each of said protein subgroups and storing resulting mass subgroup data;

analyzing said resulting mass spectra subgroup data to yield a protein profile for said diseased tissue or specimen sample;

comparing said protein profile for said diseased tissue sample or specimen against at least one protein profile from at least one normal tissue sample or specimen from said patient or other individuals; and

identifying the differences between said diseased tissue sample or specimen and said at least one protein profile for a normal tissue sample or specimen, thereby identifying protein biomarkers.

18.   A protein biomarker identified by the method of claim 17.

19.   A diagnostic method, comprising:

collecting a tissue or specimen sample from a patient;

fractionating protein content from said sample into protein subgroups;

separately performing mass spectroscopy on each of said protein subgroups and storing resulting mass subgroup data;

analyzing said resulting mass spectra subgroup data to yield a protein profile for said sample;

comparing said protein profile for said tissue sample or specimen against a protein profile library; and diagnosing presence or absence of a disease or other biological condition.